

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 17:31:49 ; Search time 20.26 Seconds
(without alignments)
430.005 Million cell updates/sec

Title: US-09-502-984B-1
Perfect score: 1194
Sequence: 1 APPPNLPDPFESKALLAA.....GGFWSAMSEPVSLTPSDLD 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 segs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	ID	Description
1	1194	100.0	508	1 EPOR_HUMAN	P19235 homo sapien
2	982.5	82.3	507	1 EPOR_MOUSE	P14753 mus musculu
3	981.5	82.2	507	1 EPOR_RAT	O07303 rattus norv
4	205	17.2	625	1 TPOR_MOUSE	O08351 mus musculu
5	185	15.5	635	1 TPOR_HUMAN	P40236 homo sapien
6	159	13.3	581	1 PRIR_BOVIN	O28172 bos taurus
7	151	12.6	581	1 PRIR_CERL	O28235 cervus elap
8	148	12.4	616	1 PRIR_RABIT	P14787 oryctolagus
9	144.5	12.1	831	1 PRIR_CHICK	O04594 gallus gall
10	136.5	11.4	830	1 PRIR_COLLI	O90374 columba liv
11	135	11.3	831	1 PRIR_MELGA	O91094 meleagris g
12	128	10.7	622	1 PRIR_HUMAN	P16471 homo sapien
13	126	10.6	522	1 IL9R_HUMAN	O01113 homo sapien
14	126	10.6	608	1 PRIR_MOUSE	O08501 mus musculu
15	123.5	10.3	634	1 GHR_MOUSE	P16882 mus musculu
16	122.5	10.3	634	1 GHR_BOVIN	P79108 bos taurus
17	121.5	10.2	634	1 GHR_SHEEP	O28575 ovis aries
18	121	10.1	610	1 PRIR_RAT	P05710 rattus norv
19	117.5	9.8	611	1 GHR_COLLI	O90375 columba liv
20	117.5	9.8	638	1 GHR_PIG	P19756 sus scrofa
21	117	9.8	608	1 GHR_CHICK	O02092 gallus gall
22	116.5	9.8	638	1 GHR_RABIT	P19941 oryctolagus
23	116	9.7	897	1 CYRB_HUMAN	P32927 homo sapien
24	113	9.5	630	1 PRIR_ORENI	O91513 oreochromis
25	111.5	9.3	1097	1 LIFR_HUMAN	P43702 homo sapien
26	108.5	9.1	976	1 GHR_RAT	P16310 rattus norv
27	107	9.0	976	1 EPB2_HUMAN	O01114 mus musculu
28	107	9.0	468	1 IL9R_MOUSE	P26311 homo sapien
29	106.5	8.9	378	1 IL3R_HUMAN	P26351 homo sapien
30	104.5	8.8	1165	1 IL6R_HUMAN	P48357 homo sapien
31	104	8.7	2594	1 LIES_DROVI	P28086 drosophila
32	102	8.5	896	1 CYRB_MOUSE	P26955 mus musculu
33	101	8.5	977	1 EPB2_MOUSE	O03145 mus musculu

34	100.5	8.4	917	1 IL6B_MOUSE	Q00560 mus musculu
35	97.5	8.2	638	1 GHR_MACMU	P79194 macaca mula
36	97.5	8.2	1092	1 LIFR_MOUSE	P42703 mus musculu
37	96	8.0	1134	1 TIE1_MOUSE	O06806 mus musculu
38	95.5	8.0	2554	1 LIES_DROME	P13368 drosophila
39	95	8.0	184	1 MPL_MPLV	P40931 myeloprolif
40	95	8.0	993	1 EPB2_MOUSE	P54763 mus musculu
41	95	8.0	1055	1 EPB2_HUMAN	P29323 homo sapien
42	94.5	7.9	551	1 IL2B_HUMAN	P14784 homo sapien
43	92.5	7.7	459	1 IL7R_MOUSE	P16872 mus musculu
44	92	7.7	369	1 CYRG_HUMAN	P31785 homo sapien
45	92	7.7	878	1 IL3B_MOUSE	P26954 mus musculu

ALIGNMENTS

RESULT 1
ID EPOR_HUMAN STANDARD: PRT: 508 AA.
AC P19235;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Erythropoietin receptor precursor (EPO-R).
GN EPOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91372359; PubMed=1654273;
RA Ehrenman K., St John T.;
RT "The erythropoietin receptor gene: cloning and identification of
RT multiple transcripts in an erythroid cell line OCIML.";
RL Exp. Hematol. 19:973-977(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90304340; PubMed=2163696;
RA Jones S.S., D'Andrea A., Haines L.L., Wong G.G.;
RT "Human erythropoietin receptor: cloning, expression, and biologic
RL characterization.";
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RC MEDLINE=92399733; PubMed=1668606;
RA Noguchi C.T., Bae K.S., Chin K., Wada Y., Schechter A.N.,
RT Harkins W.D.;
RL "Cloning of the human erythropoietin receptor gene.";
RN [4]
RP SEQUENCE OF 1-96 FROM N.A.
RX TISSUE=Placenta;
RC MEDLINE=92399734; PubMed=1668607;
RA Maoche L., Touramille C., Hattab C., Boffa G., Cartton J.P.,
RT Chretien S.;
RL "Cloning of the gene encoding the human erythropoietin receptor.";
RN [5]
RP BLOOD 78:2557-2563(1991).
RX MEDLINE=92147143; PubMed=1664413;
RA Penny L.A., Forget B.G.;
RT "Genomic organization of the human erythropoietin receptor gene.";
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 34-244.
RX MEDLINE=96291992; PubMed=8662530;
RA Livahan O., Stura E.A., Johnson D.L., Middleton S.A., Mulcahy L.S.,
RT Wright N.C., Dower W.J., Jolliffe L.K., Wilson I.A.;
RL "Functional mimicry of a protein hormone by a peptide agonist: the
RT EPO receptor complex at 2.8 A.";


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CC MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
CC AND DIFFERENTIATION.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -I- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J04843; AAA37571.1; -
DR EMBL: X53081; CAA37248.1; -
DR EMBL: M38133; AAA37572.1; -
DR EMBL: M62360; AAA37582.1; -
DR EMBL: S59388; AAB20029.2; -
DR PIR: A32385; A32385.
DR PIR: A41686; A41686.
DR PIR: S13249; S13249.
DR PIR: S14081; S14081.
DR HSSP: P19235; 1EBA.
DR MGD: MGI:95408; Epor.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR SMART: PF00041; fn3; 1.
DR SMART: SM00060; fn3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
DR Receptor: Transmembrane; Glycoprotein; Signal.
FT CHAIN 1 24
FT DOMAIN 25 507 ERYTHROPOIETIN RECEPTOR.
FT TRANSMEM 250 249 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 273 507 POTENTIAL.
FT DOMAIN 147 212 CYTOPLASMIC (POTENTIAL).
FT DISULFD 52 62 FIBRONECTIN TYPE-III.
FT DISULFD 90 106 BY SIMILARITY.
FT CARBOHD 75 75 BY SIMILARITY.
FT CONFLCT 291 291 E-N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 507 AA; 55194 MW; 067657A2E26451CA CRC64;

Query Match 82.3%; Score 982.5; DB 1; Length 507;
Best Local Similarity 83.1%; Pred. No. 5.9e-85;
Matches 187; Conservative 13; Mismatches 24; Indels 1; Gaps 1;

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DE Erythropoietin receptor precursor (EPO-R).
GN Epor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93266574; PubMed=7684373;
RA Masuda S., Nagao M., Takahata K., Konishi Y., Gallyas F.,
RA Tabira T., Sasaki R.;
RT "Functional erythropoietin receptor of the cells with neural
RT characteristics. Comparison with receptor properties of erythroid
RT cells.";
RL J. Biol. Chem. 268:11208-11216(1993).
CC -I- FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE
CC MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
CC AND DIFFERENTIATION.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -I- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL: D13566; BAA02761.1; -
DR PIR: A46713; A46713.
DR HSSP: P19235; 1EBA.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; fn3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
DR Receptor: Transmembrane; Glycoprotein; Signal.
FT CHAIN 1 24
FT SIGNAL 1 24 BY SIMILARITY.
FT CHAIN 25 507 ERYTHROPOIETIN RECEPTOR.
FT DOMAIN 25 249 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 250 272 POTENTIAL.
FT DOMAIN 273 507 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 147 212 FIBRONECTIN TYPE-III.
FT DISULFD 52 62 BY SIMILARITY.
FT DISULFD 90 106 BY SIMILARITY.
FT CARBOHD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 507 AA; 55499 MW; AC79AF22D06A7312 CRC64;

Query Match 82.2%; Score 981.5; DB 1; Length 507;
Best Local Similarity 82.7%; Pred. No. 7.4e-85;
Matches 186; Conservative 15; Mismatches 23; Indels 1; Gaps 1;

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RESULT 4
TPOR_MOUSE STANDARD; PRT; 625 AA.
ID TPOR_MOUSE
AC 008351;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thrombopoietin receptor precursor (Tpo-R) (Myeloproliferative leukemia
DE protein) (C-mpl).
GN MPL OR TPOR.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=93327753; PubMed=8334987;
RA Skoda R.C., Seidlin D.C., Chiang M.K., Peichel C.L., Vogt T.F.,
RA Leder P.;
RT "Murine c-mpl: a member of the hematopoietic growth factor receptor
RT superfamily that transduces a proliferative signal.";
RL EMBO J. 12:2645-2653(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ICEM; TISSUE=Fetal liver;
RX MEDLINE=93390934; PubMed=8397366;
RA Vigon I., Florindo C., Richelson S., Guenet J.-L., Mattei M.-G.,
RA Souvri I.M., Cosman D., Gisselbrecht S.;
RT "Characterization of the murine Mpl proto-oncogene, a member of the
RT hematopoietic cytokine receptor family: molecular cloning,
RT chromosomal location and evidence for a function in cell growth.";
RL Oncogene 8:2607-2615(1993).
CC -1- FUNCTION: RECEPTOR FOR THROMBOPOIETIN. MAY REPRESENT A REGULATORY
CC MOLECULE SPECIFIC FOR TPO-R-DEPENDENT IMMUNE RESPONSES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; 222649; CA80365.1; -
DR EMBL; 222657; CA80372.1; -
DR EMBL; X73677; CA85203.1; -
DR PIR; S35317; S35317.
DR HSSP; P19235; IEBA.
DR MGD; MGI:97076; MPL.
DR InterPro: IPR002996; CRA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 625 THROMBOPOIETIN RECEPTOR.
FT DOMAIN 26 482 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 483 504 POTENTIAL.
FT DOMAIN 505 625 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 117 117 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CONFLICT 2 8 MISSING (IN REF. 2).
FT CONFLICT 99 99 D -> V (IN REF. 2).
FT CONFLICT 222 222 P -> PVRTSPAGE (IN REF. 2).
SQ SEQUENCE 625 AA; 69817 MW; 309CF6EAA3724549 CRC64;

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Query Match 17.2%; Score 205; DB 1; Length 625;
Best Local Similarity 25.9%; Pred. No. 1.2e-11;

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Matches 66; Conservative 29; Mismatches 112; Indels 48; Gaps 7;
QY 13 SKAALLAARGPEELLCTFERLEDVLCFWEBAASAGVPGNYSFQLEDEPMKICRLHOA 72
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 25 SDVFFLLALGTEDPLNCFQSFEDLTCFMBDEEAA--PSGTQLLYAVRREKPRACPLYGQ 82
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 73 PTAKGAVRWGCSLPTAD-TSSFPLRLRYTAAS-GAPRHRVHINEVYLLDAPVGLVAR 130
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 83 SVPTFGTRVYCCFPADDEVRLFFPLHLWKNVSLNLTGLRVLEFVSGLPAPPRVIKAR 142
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 131 LADESGHVLRW-LPPETP--MTSHIRYEDVVSAGNGASVOREILBGR----- 179
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 143 GGSQPELOIHWEAPAPETSDPLRHLRIGPTDSSNATAPSV--IQLSTETCCPTLMP 200
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 180 -----ECVLSNLGRRTYTPAVBARNAEPSFGF 208
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 201 NPVPVLDPPCVHPRTASOPHPAPFLTVKGSGLVGLQASKSYMLQSLRSPDGVSLRGS 260
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 209 WSAWSEPVSLTPSD 223
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 261 WGPWSEPVTVLDLPGD 275

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RESULT 5
TPOR_HUMAN STANDARD; PRT; 635 AA.
ID TPOR_HUMAN
AC P40238;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thrombopoietin receptor precursor (Tpo-R) (Myeloproliferative leukemia
DE protein) (C-mpl) (CD110 antigen).
GN MPL OR TPOR.
OS Homo sapiens (Human).
OC Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=92302297; PubMed=1608974;
RA Vigon I., Morron J.-P., Cocault L., Mitjavila M.-T., Tambourin P.,
RA Gisselbrecht S., Souvri M.;
RT "Molecular cloning and characterization of MPL, the human homolog of
RT the v-mpl oncogene: identification of a member of the hematopoietic
RT growth factor receptor superfamily.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:5640-5644(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94292186; PubMed=8020956;
RA Mignotte V., Vigon I., de Crevecoeur E., Romeo P.H., Lemarchandel V.,
RA Chretien S.;
RT "Structure and transcription of the human c-mpl gene (MPL).";
RL Genomics 20:5-12(1994).
CC -1- FUNCTION: RECEPTOR FOR THROMBOPOIETIN. MAY REPRESENT A REGULATORY
CC MOLECULE SPECIFIC FOR TPO-R-DEPENDENT IMMUNE RESPONSES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: C-MPL-K (SHOWN HERE) AND C-MPL-
CC P; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT A LOW LEVEL IN A LARGE NUMBER OF
CC CELLS OF HEMATOPOIETIC ORIGIN. THE TWO FORMS (C-MPL-K AND C-MPL-
CC P) ARE ALWAYS FOUND TO BE COEXPRESSED.
CC -1- DISEASE: DEFECTS IN MPL ARE A CAUSE OF CONGENITAL AMEGAKARYOCYTIC
CC THROMBOCYTOPENIA (CAMT); A DISEASE CHARACTERIZED BY ISOLATED
CC THROMBOCYTOPENIA AND MEGAKARYOCYTOPENIA WITH NO PHYSICAL
CC ANOMALIES.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-8 IS THE INITIATOR.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD10 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/11586825.g.htm".
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70 CERNROE NOCITL SNNHSDIMMAYIYVNNXNGMOLOODEEL VHNATTEEEEN AYA

BU

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Oy 126 GVALU-----ADSSGIVUVRMLPPEPTPMTSH---IRYEVDSAGNAGSAGVQVVELLEGR 179
Db 132 NLTELEKHPEDRKPLMLINKMSPPMTDYKSGCFITQYERLRKPEKATDMEHFTLKQ--T 189
Oy 180 ECVSLNLGRRTTYTFAVARMAEPSEFGGFWSAMSEPVSLPPSD 223
Db 190 QKIFINLPQGGOKYLVQIRCK---PDH-GYWMSEWSPSSSIOIPND 229

RESULT 7
PRLR_CEREL STANDARD; PRT; 581 AA.
AC Q28235;
AD 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE prolactin receptor precursor (PRL-R).
GN PRLR.
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
OC NCBI_Taxid=9860;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96030711; Pubmed=7561644;
RA Clarke L.A., Edey M., Loudon A.S., Randall V.A., Postal-Vlnay M.C.,
RA Kelly P.A., Jabour H.N.;
RT "Expression of the prolactin receptor gene during the breeding and
RT non-breeding seasons in red deer (Cervus elaphus): evidence for the
RT expression of two forms in the testis.";
RL J. Endocrinol. 146:313-321(1995).
CC -! FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -! SUBCELLULAR LOCATION: Type I membrane protein.
CC -! SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -! SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC CC -----
CC CC EMBL; X94953; CAA64419.1; -.
CC CC HSSP; P14787; IAN3.
CC CC InterPro; IPR002996; CRIA.
CC CC InterPro; IPR003961; FN.III.
CC CC InterPro; IPR003528; Hematopo_receptor_L.F1.
CC CC Pfam; PF00041; In3; 2.
CC CC SMART; SM00060; FN3; 1.
CC CC PROSITE; PS01352; HEMATOPO_REC_L.F1; 1.
CC CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
CC CC SIGNAL 1 24
CC CC CHAIN 1 581
CC CC DOMAIN 25 234
CC CC TRANSMEM 235 258
CC CC DOMAIN 259 581
CC CC DOMAIN 25 122
CC CC DOMAIN 123 227
CC CC DISULFD 36 46
CC CC DISULFD 75 86
CC CC CARBOHD 59 59
CC CC CARBOHD 132 132
CC CC CARBOHD 233 233
CC CC SEQUENCE 581 AA; 65159 MW; 975E47CB3CF28EC CRC64;

Query Match 12.6%; Score 151; DB 1; Length 581;
Best Local Similarity 23.9%; Pred. No. 1.3e-06; .

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Matches 51. Conservative 36. Mismatches 100. Indels 26. Gaps 9
OY 23 PEEELICFERLEDLYCFMEDEAASAGVGNYSFSQLEDDEPMKLCRLQAPFARAVAFW 82
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 31 PPIIKCRSPGKRTKFCWMEPGSDGL-PLNYLLIYHKGE-----TLIECDPKGPGNT 85
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 83 CSLPADIASSFPEPLRLRYTA-----ASGAPRYHNVHINIEVLLDADVGLVARL---AD 133
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 86 CYFSKHKHSIMKIYIYTNAINQMGVSSDPLY---VDYTYVEEPERANLLTELKHEED 142
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 134 ESGHVLVAMLPPEPEPMYS---HIREVDVSGNGAGSVQRYVEILGTECVLSMLRBT 190
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 143 RKPYLMIMWFPEPTLLDVDSGWMFIQYELRLKRETAAD--WEIHFAAKOTQDKITSLYPGQ 200
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 191 RYTFAVRARMAEPSEFGFMSAMSEPVSLTSPSD 223
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 201 KLVQVRCCK---PDH-GYVSEKSPSSSIQIPND 229
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
PRLR_RABIT
ID PRLR_RABIT STANDARD; PRT; 616 AA.
PI4787.
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN PRLR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
   (1)
RN RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=89184578; PubMed=2928321;
RA Edery M., Jolicoeur C., Levi-Meynuel C., Dusanter-Fourt I.,
RA Perlidou B., Boutin J.M., Lesueur L., Kelly P.A., Djiane J.;
RT "Identification and sequence analysis of a second form of prolactin
RT receptor by molecular cloning of complementary DNA from rabbit
RT mammary gland.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:2112-2116(1989).
RN [2]
RP 3D-STRUCTURE MODELING OF 30-228.
RX MEDLINE=97248733; PubMed=9094747;
RA Halaby D., Thoreau E., Djiane J., Mornon J.P.;
RT "Homology modeling of rabbit prolactin hormone complexed with its
RT receptor.";
RL Proteins 27:459-468(1997).
CC -I- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -I- SIMILARITY: CONTAINS 2 FIBROCTIN TYPE III-LIKE DOMAINS.
-----
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DR EMBL: J04510; AAA31457.1; -.
DR PIR: A30304; A30304
DR PDB: 1AN3; 03-DEC-97.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR Pfam: PF00041; fn3; 2
DR SMART: SM00060; FN3; 2.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat; 3D-structure.

```

	RESULT	10
PRLR_COLLI	ID	
AC	Q90374;	STANDARD; PRT; 830 AA.
DT	01-NOV-1997 (Rel. 35, Created)	
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	15-JUL-1998 (Rel. 36, Last annotation update)	
DE	Prolactin receptor precursor (PRL-R).	
GN	PRLR.	
OS	Columba livia (Domestic pigeon).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Archosauria; Aves; Neognathae; Columbiformes; Columbiidae; Columba.	
OX	NCBI_TaxID=8932;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Cropsac;	
RX	MEDLINE=94283267; PubMed=7516866;	
RA	Chen X., Horseman N.D.;	
RT	"Cloning, expression, and mutational analysis of the pigeon prolactin	
TT	receptor.";	

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 CC -----
 DR EMBL: L13593; AAC37641.1; -
 DR EMBL: L14811; AAA02686.1; -
 DR EMBL: D10214; BAA01066.1; -
 DR EMBL: X73372; CAA51789.1; -
 DR EMBL: M22959; AAA39976.1; -
 DR EMBL: M22958; AAA39976.1; -
 DR PIR: J0671; J0671.
 DR HSSP: P14787; IAN3.
 DR MGD: MGI:97763; Pr1r.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR003528; Hematopo_receptor_L_F1.
 DR Pfam: PF00041; FN3; 2.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KW Alternative splicing.
 FT SIGNAL 1 19
 FT CHAIN 20 608
 FT DOMAIN 20 229
 FT TRANSMEM 230 253
 FT DOMAIN 254 608
 FT DOMAIN 20 117
 FT DOMAIN 119 222
 FT DISULFID 31 41
 FT DISULFID 70 81
 FT CARBOHYD 54 54
 FT CARBOHYD 99 99
 FT CARBOHYD 127 127
 FT VANSPLIC 281 292
 FT VANSPLIC 293 608
 FT VANSPLIC 281 303
 FT VANSPLIC 304 608
 FT CONFLICT 558 558
 FT SEQUENCE 608 AA; 68240 MW; B8CE202B2E9CF6C CRC64;
 Query Match 10.6%; Score 126; DB 1; Length 608;
 Best Local Similarity 22.3%; Pred. No. 0.00032;
 Matches 47; Conservative 38; Mismatches 104; Indels 22; Gaps 8;
 QY 23 PELLCTERLELDVCFWEAASAGVGENYSFQLEDEPMKLCRLHQAPTARGAVRFW 82
 DB 26 PEIHCRCSPDKETFTCMWPGSDGGL-PTNYSILTVSKGEK-----NTYCPDYKTSGPSNS 80
 QY 83 GSLPTADTSSEFVLELRVTA-----ASGAPRYHRIHINEVVLADAPGL---VARLAD 133
 DB 81 CFFSQYVTSIMKITYITVATNMGSSISDPL---VDVTYVLEPPPNLLEVKQLKD 137
 QY 134 ESGHVVLRMLPPETPM-TSHIRYEDVASAGNAGSVQVEILEGTECVLSNLGRTRY 192
 DB 138 KTYLWVKMLPPTITDVKKGWFTMEYELRLKSEADENWIHTGTQTKVYDLYGQKY 197
 QY 193 TFAVRAKMAEFSFGFWSAMSEPVSLTFSD 223
 DB 198 LVOTRCK--PDH-GYWSRMGQEKSIETFPND 224
 RESULT 15
 GHR_MOUSE STANDARD; PRT; 650 AA.
 ID GHR_MOUSE P16882; P16590; Q9R264;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Growth hormone receptor precursor (Gh receptor) (Gh binding protein)
 DE (GHRP) (Serum binding protein).

GN GHR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=89295449; PubMed=2739661;
 RA Smith W.C., Kuniyoshi J., Talamantes F.;
 RT "Mouse serum growth hormone (GH) binding protein has GH receptor
 RT extracellular and substituted transmembrane domains";
 RL Mol. Endocrinol. 3:984-990(1989).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=Swiss Webster, and DBA/2J;
 RX MEDLINE=99367316; PubMed=10425445;
 RA Moffat J.G., Edens A., Talamantes F.;
 RT "Structure and expression of the mouse growth hormone receptor/growth
 RT hormone binding protein gene";
 RL J. Mol. Endocrinol. 23:33-44(1999).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=Swiss Webster, and DBA/2J;
 RX MEDLINE=95080157; PubMed=7988474;
 RA Edens A., Southard J.N., Talamantes F.;
 RT "Mouse growth hormone receptor/binding protein and growth hormone
 RT receptor transcripts are produced from a single gene by alternative
 RT splicing";
 RL Endocrinology 135:2802-2805(1994).
 RN [4]
 RP SEQUENCE OF 156-650 FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL;
 RX MEDLINE=95201642; PubMed=7894338;
 RA Zhou Y., He L., Kopechick J.J.;
 RT "An exon encoding the mouse growth hormone binding protein (mGHRP)
 RT carboxy terminus is located between exon 7 and 8 of the mouse growth
 RT hormone receptor gene";
 RL Receptor 4:223-227(1994).
 RN [5]
 RP REVISIONS.
 RC STRAIN=C57BL;
 RA Zhou Y., He L., Kopechick J.J.;
 RL Submitted (FEB-1996) to the EMBL/Genbank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 25-41.
 RX MEDLINE=88288223; PubMed=3398846;
 RA Smith W.C., Colosi P., Talamantes F.;
 RT "Isolation of two molecular weight variants of the mouse growth
 RT hormone receptor";
 RL Mol. Endocrinol. 2:108-116(1988).
 CC -1- FUNCTION: Isoform 1 is a receptor for pituitary gland growth
 CC hormone. Isoform 2 is a serum growth hormone binding protein that
 CC may play an important role in regulating the effective serum
 CC concentration of gh.
 CC -1- SUBUNIT: Isoform 1 is a homodimer.
 CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein (isoform 1);
 CC secreted (isoform 2).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1/mmw GHR (shown here) and 2/LMW
 CC GHR; are produced by alternative splicing.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTRAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC -----
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 CC -----
 DR EMBL: M33324; AAA37690.1; ALT_SEQ.
 DR EMBL: M31680; AAA37689.1; ALT_SEQ.
 DR EMBL: AF120489; AAD32556.1; -.

DR EMBL; AF120481; AAD32556.1; JOINED.
DR EMBL; AF120482; AAD32556.1; JOINED.
DR EMBL; AF120483; AAD32556.1; JOINED.
DR EMBL; AF120484; AAD32556.1; JOINED.
DR EMBL; AF120485; AAD32556.1; JOINED.
DR EMBL; AF120486; AAD32556.1; JOINED.
DR EMBL; AF120487; AAD32556.1; JOINED.
DR EMBL; AF120488; AAD32556.1; JOINED.
DR EMBL; AF120487; AAD32555.1; JOINED.
DR EMBL; AF120481; AAD32555.1; JOINED.
DR EMBL; AF120482; AAD32555.1; JOINED.
DR EMBL; AF120483; AAD32555.1; JOINED.
DR EMBL; AF120484; AAD32555.1; JOINED.
DR EMBL; AF120485; AAD32555.1; JOINED.
DR EMBL; AF120486; AAD32555.1; JOINED.
DR EMBL; U49266; AAK62802.1; JOINED.
DR EMBL; U49268; AAK62802.1; JOINED.
DR EMBL; U43933; AAK62802.1; JOINED.
DR HSSP; P10912; 1HWI.
DR MGD; MGI:95708; Ghr.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; Hematopo_receptor_L_F1.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
FT SIGNAL 1 24
FT CHAIN 25 650
FT DOMAIN 25 273
FT TRANSMEM 274 297
FT DOMAIN 298 650
FT DOMAIN 153 260
FT DISULFID 56 66
FT DISULFID 109 120
FT DISULFID 134 148
FT CARBOHYD 123 123
FT CARBOHYD 164 164
FT CARBOHYD 169 169
FT CARBOHYD 208 208
FT CARBOHYD 271 296
FT VARSPLIC 297 650
FT CONFLICT 25 25
FT CONFLICT 162 162
FT CONFLICT 325 325
FT CONFLICT 423 423
SQ SEQUENCE 650 AA; 72783 MW; 9565380CAF0B931 CRC64;
GROWTH HORMONE RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
DIOFPWFLIIIGIFGVAWLEVFVIR -> GTRKSNQHPHO
EIDNHLXHOLRIH (IN ISOFORM 2).
MISSING (IN ISOFORM 2).
T -> A (IN REF. 6).
G -> A (IN REF. 3 AND 4).
E -> G (IN REF. 2).
R -> A (IN REF. 2).

Query Match 10.3%; Score 123.5; DB 1; Length 650;
Best Local Similarity 22.6%; Pred. No. 0.0006;
Matches 52; Conservative 39; Mismatches 88; Indels 51; Gaps 10;

QY 23 PELLLEFTEFLIEDLVCFWEEAASAGV-GPGNYSFSQLEDEPDKICR 68
DB 51 PRTTKCRSPLELEFFSCWTEGDNPDILKTPESIOLYTAKKRESQROARIAHEMTQEWREC- 109
QY 69 LHOAPTARGAVRWCSPFTADTSSFPVLELRYTASGAPRYHRVHIINEVLLDAPVGLV 128
DB 110 ---PDYVSAKNSCYFNSYTSIMWPCIKL-TNGDLLDQKCFYVDEIVQDPPIGLN 164
QY 129 ARLADES---GHVVLRLPLPETPMTSH---IREVDVSAGNGAGSVORVEILGR-- 178
DB 165 WTLINISLIGIRGDIQVSMQPPNADVLKGMILLEYE-----IQYKEVNESKWK 213
QY 179 -----TECVLSNLGRRTYTFAVARARMAEPFGGFWSAMSEPVSLTLP 221
DB 214 VMGPWLTYCPVYSLRDKKEHYVRSR-QRSFEKY-SESEVELRVIFP 260

Search completed: August 28, 2002, 17:40:41
Job time: 532 sec